

Claims

1. (currently amended) A purified polynucleotide comprising a nucleotide sequence encoding a full-length mutant polypeptide of large subunit of a plant maize ADP-glucose pyrophosphorylase polypeptide large subunit, or a biologically active fragment of said full-length mutant polypeptide, wherein said full-length mutant polypeptide or said fragment of said full-length mutant polypeptide comprises an amino acid mutation in the amino acid sequence of said polypeptide maize ADP-glucose pyrophosphorylase large subunit, and wherein when said full-length mutant polypeptide or said fragment of said full-length mutant polypeptide is expressed to form a mutant ADP-glucose pyrophosphorylase enzyme, said mutant enzyme, or a fragment of said mutant enzyme, exhibits increased heat stability relative to the wild type ADP-glucose pyrophosphorylase enzyme.

2-41. (canceled)

42. (currently amended) The polynucleotide according to claim 1, wherein said mutant polypeptide encoded by said polynucleotide comprises an amino acid mutation wherein the amino acid corresponding to histidine at position 333 in the amino acid sequence of the wild type large subunit of ADP-glucose pyrophosphorylase polypeptide of maize is replaced by an amino acid that confers said increased heat stability on said mutant enzyme.

43. (currently amended) The polynucleotide according to claim 42, wherein said amino acid corresponding to histidine at position 333 is replaced with a phenylalanine.

44. (currently amended) The polynucleotide according to claim 42, wherein said amino acid corresponding to histidine at position 333 is replaced with a methionine.

45. (previously presented) The polynucleotide according to claim 1, wherein said mutant polypeptide encoded by said polynucleotide further comprises an amino acid mutation that confers increased seed weight to a plant expressing said polynucleotide.

46. (previously presented) The polynucleotide according to claim 45, wherein said polynucleotide comprises the *Rev6* mutation.

47. (currently amended) The polynucleotide according to claim 45, wherein said mutation comprises the insertion of at least one serine residue between ~~amino acids corresponding to positions the glycine at position 494 and the tyrosine at position 495~~ in the amino acid sequence of the wild type large subunit of ADP-glucose pyrophosphorylase polypeptide of maize.

48. (currently amended) The polynucleotide according to claim 45, wherein said mutation comprises the insertion of the amino acid pair tyrosine:serine between ~~amino acids corresponding to positions the glycine at position 494 and the tyrosine at position 495~~ in the amino acid sequence of the wild type large subunit of ADP-glucose pyrophosphorylase polypeptide of maize.

49. (currently amended) The polynucleotide according to claim 45, wherein said mutation comprises the insertion of the amino acid pair serine:tyrosine between ~~amino acids corresponding to positions the tyrosine at position 495 and the tyrosine at position 496~~ in the amino acid sequence of the wild type large subunit of ADP-glucose pyrophosphorylase polypeptide of maize.

50-54. (canceled)

55. (currently amended) The polynucleotide according to claim 1, wherein said mutant polypeptide encoded by said polynucleotide comprises an amino acid mutation wherein the ~~amino acid corresponding to leucine at position 426~~ of the wild type large subunit of ADP-glucose pyrophosphorylase polypeptide of maize is replaced by a phenylalanine amino acid and the ~~amino acid corresponding to alanine at position 177~~ of the wild type large subunit of ADP-glucose

pyrophosphorylase polypeptide of maize is replaced by an amino acid that confers said increased heat stability on said mutant enzyme.

56. (currently amended) The polynucleotide according to claim 55, wherein said ~~amino-acid corresponding to alanine at position 177~~ is replaced with a proline.

57. (currently amended) The polynucleotide according to claim 55, wherein said ~~amino-acid corresponding to alanine at position 177~~ is replaced with a valine.

58. (currently amended) The polynucleotide according to claim 1, wherein said mutant polypeptide encoded by said polynucleotide comprises an amino acid mutation wherein the ~~amino acid corresponding to glutamic acid at position 324~~ of the wild type large subunit of ADP-glucose pyrophosphorylase polypeptide of maize is replaced by a lysine amino acid, and the ~~amino-acid corresponding to alanine at position 359~~ of the wild type large subunit of ADP-glucose pyrophosphorylase polypeptide of maize is replaced by a valine amino acid, and the ~~amino-acid corresponding to alanine at position 396~~ of the wild type large subunit of ADP-glucose pyrophosphorylase polypeptide of maize is replaced by an amino acid that confers said increased heat stability on said mutant enzyme.

59. (currently amended) The polynucleotide according to claim 58, wherein said ~~amino-acid corresponding to alanine at position 396~~ is replaced with a valine.

60. (previously presented) A method for increasing resistance of a plant to heat stress conditions, said method comprising incorporating the polynucleotide of claim 1 into the genome of said plant and expressing the protein encoded by said polynucleotide molecule.

61. (previously presented) The method according to claim 60, wherein said plant is a monocotyledonous plant.

62. (previously presented) The method according to claim 61, wherein said monocotyledonous plant is selected from the group consisting of rice, wheat, barley, oats, sorghum, maize, lily, and millet.

63. (previously presented) The method according to claim 60, wherein said plant is *Zea mays*.

64. (previously presented) The method according to claim 60, wherein said plant is a dicotyledonous plant.

65. (previously presented) The method according to claim 64, wherein said dicotyledonous plant is selected from the group consisting of pea, alfalfa, chickpea, chicory, clover, kale, lentil, soybean, tobacco, potato, sweet potato, radish, cabbage, rape, apple tree, and lettuce.

66. (currently amended) The method according to claim 60, wherein said mutant polypeptide encoded by said polynucleotide comprises an amino acid mutation wherein the amino acid corresponding to leucine at position 426 of the wild type large subunit of ADP-glucose pyrophosphorylase polypeptide of maize is replaced by a phenylalanine amino acid and the amino acid corresponding to alanine at position 177 of the wild type large subunit of ADP-glucose pyrophosphorylase polypeptide of maize is replaced by an amino acid that confers said increased heat stability on said mutant enzyme.

67. (currently amended) The method according to claim 66, wherein said amino acid corresponding to alanine at position 177 is replaced with a proline.

68. (currently amended) The method according to claim 66, wherein said acid corresponding to alanine at position 177 is replaced with a valine.

69. (currently amended) The method according to claim 60, wherein said mutant polypeptide encoded by said polynucleotide comprises an amino acid mutation wherein the amino acid corresponding to glutamic acid at position 324 of the wild type large subunit of ADP-glucose pyrophosphorylase polypeptide of maize is replaced by a lysine amino acid, and the amino acid corresponding to alanine at position 359 of the wild type large subunit of ADP-glucose pyrophosphorylase polypeptide of maize is replaced by a valine amino acid, and the amino acid corresponding to alanine at position 396 of the wild type large subunit of ADP-glucose pyrophosphorylase polypeptide of maize is replaced by an amino acid that confers said increased heat stability on said mutant enzyme.

70. (currently amended) The method according to claim 69, wherein said amino acid corresponding to alanine at position 396 is replaced with a valine.

71. (previously presented) The method according to claim 60, wherein said mutant polypeptide encoded by said polynucleotide further comprises an amino acid mutation that confers increased seed weight to a plant expressing said polynucleotide.

72. (previously presented) A plant or plant tissue comprising the polynucleotide molecule of claim 1.

73. (previously presented) The plant or plant tissue according to claim 72, wherein said plant or plant tissue is monocotyledonous.

74. (previously presented) The plant or plant tissue according to claim 73, wherein said monocotyledonous plant or plant tissue is selected from the group consisting of rice, wheat, barley, oats, sorghum, maize, lily, and millet.

75. (previously presented) The plant or plant tissue according to claim 72, wherein said plant is *Zea mays* or said plant tissue is from *Zea mays*.

76. (previously presented) The plant or plant tissue according to claim 72, wherein said plant or plant tissue is dicotyledonous.

77. (previously presented) The plant or plant tissue according to claim 76, wherein said dicotyledonous plant or plant tissue is selected from the group consisting of pea, alfalfa, chickpea, chicory, clover, kale, lentil, soybean, tobacco, potato, sweet potato, radish, cabbage, rape, apple tree, and lettuce.

78. (previously presented) The plant tissue according to claim 72, wherein said plant tissue is a seed.

79. (currently amended) The plant or plant tissue according to claim 72, wherein said mutant polypeptide encoded by said polynucleotide comprises an amino acid mutation wherein the ~~amino acid corresponding to leucine at~~ position 426 of the wild type large subunit of ADP-glucose pyrophosphorylase polypeptide of maize is replaced by a phenylalanine amino acid and the ~~amino acid corresponding to alanine at~~ position 177 of the wild type large subunit of ADP-glucose pyrophosphorylase polypeptide of maize is replaced by an amino acid that confers said increased heat stability on said mutant enzyme.

80. (currently amended) The plant or plant tissue according to claim 79, wherein said ~~amino acid corresponding to alanine at~~ position 177 is replaced with a proline.

81. (currently amended) The plant or plant tissue according to claim 79, wherein said ~~amino acid corresponding to alanine at~~ position 177 is replaced with a valine.

82. (currently amended) The plant or plant tissue according to claim 72, wherein said mutant polypeptide encoded by said polynucleotide comprises an amino acid mutation wherein the ~~amino acid corresponding to glutamic acid at~~ position 324 of the wild type large subunit of ADP-glucose

pyrophosphorylase polypeptide of maize is replaced by a lysine amino acid, and the amino acid corresponding to alanine at position 359 of the wild type large subunit of ADP-glucose pyrophosphorylase polypeptide of maize is replaced by a valine amino acid, and the amino acid corresponding to alanine at position 396 of the wild type large subunit of ADP-glucose pyrophosphorylase polypeptide of maize is replaced by an amino acid that confers said increased heat stability on said mutant enzyme.

83. (currently amended) The plant or plant tissue according to claim 82, wherein said amino acid corresponding to alanine at position 396 is replaced with a valine.

84. (previously presented) The plant or plant tissue according to claim 72, wherein said mutant polypeptide encoded by said polynucleotide further comprises an amino acid mutation that confers increased seed weight to a plant expressing said polynucleotide.

85. (new) The method according to claim 71, wherein said polynucleotide comprises the *Rev6* mutation.

86. (new) The method according to claim 71, wherein said mutation comprises the insertion of at least one serine residue between the glycine at position 494 and the tyrosine at position 495 in the amino acid sequence of the wild type large subunit of ADP-glucose pyrophosphorylase polypeptide of maize.

87. (new) The method according to claim 71, wherein said mutation comprises the insertion of the amino acid pair tyrosine:serine between the glycine at position 494 and the tyrosine at position 495 in the amino acid sequence of the wild type large subunit of ADP-glucose pyrophosphorylase polypeptide of maize.

88. (new) The method according to claim 71, wherein said mutation comprises the insertion of the amino acid pair serine:tyrosine between the tyrosine at position 495 and the tyrosine at

position 496 in the amino acid sequence of the wild type large subunit of ADP-glucose pyrophosphorylase polypeptide of maize.

89. (new) The plant or plant tissue according to claim 84, wherein said polynucleotide comprises the *Rev6* mutation.

90. (new) The plant or plant tissue according to claim 84, wherein said mutation comprises the insertion of at least one serine residue between the glycine at position 494 and the tyrosine at position 495 in the amino acid sequence of the wild type large subunit of ADP-glucose pyrophosphorylase polypeptide of maize.

91. (new) The plant or plant tissue according to claim 84, wherein said mutation comprises the insertion of the amino acid pair tyrosine:serine between the glycine at position 494 and the tyrosine at position 495 in the amino acid sequence of the wild type large subunit of ADP-glucose pyrophosphorylase polypeptide of maize.

92. (new) The plant or plant tissue according to claim 84, wherein said mutation comprises the insertion of the amino acid pair serine:tyrosine between the tyrosine at position 495 and the tyrosine at position 496 in the amino acid sequence of the wild type large subunit of ADP-glucose pyrophosphorylase polypeptide of maize.